The specification has been amended to correct clerical errors and to remove hyperlinks to the world-wide-web.

Claims 25, 29, and 36 were canceled without prejudice or disclaimer.

Claims 24, 27, 28, 31-34, and 37-39 were amended. Thus, Claims 24, 26-28, 30-35, and 37-39 are pending in the application. The claims were amended to correct minor clerical errors and to express more clearly that which Applicants consider their invention. Support for the amendments are found in the specification as filed. For example, Claim 24 was amended to include the limitations of Claims 25 and 29 and to remove the SEQ ID NOs of the sequences not being claimed.

Claims 27, 28 were clarified and the SEQ ID NOs not being claimed were removed.

Claim 36 was cancelled as being drawn to non-elected material.

No new matter is believed to have been introduced.

A version with markings to show changes made is attached.

A petition for a one-month extension of time is also attached.

It is respectfully submitted that the claims are now in form for allowance which allowance is respectfully requested.

Please charge any fees associated with the filing of this response to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company). If the fee is insufficient or incorrect, please charge or credit the balance to the above-identified deposit account.

Respectfully submitted,

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Dated: October 31, 2002

Version With Markings to Show Changes Made

In showing the changes, deleted material is bracketed, and inserted material is shown as underlined.

IN THE SPECIFICATION

Please replace the following paragraphs:

Paragraph starting on page 2 at line 33:

It is preferred that the isolated polynucleotide of the claimed invention consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38. The present invention also relates to an isolated polynucleotide comprising a nucleotide sequence[s] of at least [one of]60 (preferably at least [one of]40, most preferably at least [one of]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 and the complement of such nucleotide sequences.

Paragraph starting on page 3 at line 28:

The present invention relates to a method of obtaining a nucleic acid fragment encoding a substantial portion of an Mlo homolog polypeptide gene, preferably a plant Mlo homolog polypeptide gene, comprising the steps of : synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least [one of]60 (preferably at least [one of]40, most preferably at least [one of]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a portion of an Mlo homolog amino acid sequence.

Paragraph starting on page 4 at line 9:

The present invention relates to an isolated polynucleotide of the present invention comprising at least [one of]35 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37.

Paragraph starting on page 5 at line 14:

In the context of this disclosure, a number of terms shall be utilized. As used herein, a "polynucleotide" is a nucleotide sequence such as a nucleic acid fragment. A polynucleotide may be a polymer of RNA or DNA that is single- or double-stranded, that optionally contains synthetic, non-natural or altered nucleotide bases. A

polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA, synthetic DNA, or mixtures thereof. An isolated polynucleotide of the present invention may include at least [one of]60 contiguous nucleotides, preferably at least [one of]40 contiguous nucleotides, most preferably [one of]at least 30 contiguous nucleotides derived from SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, or the complement of such sequences.

Paragraph starting on page 6 at line 29:

Substantially similar nucleic acid fragments may be selected by screening nucleic acid fragments representing subfragments or modifications of the nucleic acid fragments of the instant invention, wherein one or more nucleotides are substituted, deleted and/or inserted, for their ability to affect the level of the polypeptide encoded by the unmodified nucleic acid fragment in a plant or plant cell. For example, a substantially similar nucleic acid fragment representing at least [one of]30 contiguous nucleotides derived from the instant nucleic acid fragment can be constructed and introduced into a plant or plant cell. The level of the polypeptide encoded by the unmodified nucleic acid fragment present in a plant or plant cell exposed to the substantially similar nucleic fragment can then be compared to the level of the polypeptide in a plant or plant cell that is not exposed to the substantially similar nucleic acid fragment.

Paragraph starting on page 7 at line 3:

For example, it is well known in the art that antisense suppression and co-suppression of gene expression may be accomplished using nucleic acid fragments representing less than the entire coding region of a gene, and by nucleic acid fragments that do not share 100% sequence identity with the gene to be suppressed. Moreover, alterations in a nucleic acid fragment which result in the production of a chemically equivalent amino acid at a given site, but do not affect the functional properties of the encoded polypeptide, are well known in the art. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a functionally equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal portions of the polypeptide molecule would also not be expected to alter the activity of the polypeptide. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity of the encoded

products. Consequently, an isolated polynucleotide comprising a nucleotide sequence of at least [one of]60 (preferably at least [one of]40, most preferably at least [one of]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, or the complement of such nucleotide sequences may be used in methods of selecting an isolated polynucleotide that affects the expression of a polypeptide (an Mlo homolog) in a host cell. A method of selecting an isolated polynucleotide that affects the level of expression of a polypeptide in a host cell (eukaryotic, such as plant or yeast, prokaryotic such as bacterial, or viral) may comprise the steps of: constructing an isolated polynucleotide of the present invention or an isolated chimeric gene of the present invention; introducing the isolated polynucleotide or the isolated chimeric gene into a host cell; measuring the level a polypeptide in the host cell containing the isolated polynucleotide; and comparing the level of a polypeptide in the host cell containing the isolated polynucleotide with the level of a polypeptide in a host cell that does not contain the isolated polynucleotide.

Paragraph starting on page 8 at line 31:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as

reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph starting on page 13 at line 19:

In addition, two short segments of the instant nucleic acid fragments may be used in polymerase chain reaction protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. The polymerase chain reaction may also be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the instant nucleic acid fragments, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, the skilled artisan can follow the RACE protocol (Frohman et al. (1988) *Proc. Natl. Acad. Sci. USA 85*:8998-9002) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the instant sequences. Using commercially available 3' RACE or 5' RACE systems (BRL), specific 3' or 5' cDNA fragments can be isolated (Ohara et al. (1989) *Proc. Natl. Acad. Sci. USA 86*:5673-5677; Loh et al. (1989) *Science 243*:217-220). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman and Martin (1989) *Techniques 1*:165). Consequently, a polynucleotide comprising a nucleotide sequence of at least [one of]60 (preferably [one of]at least 40, most preferably [one of]at least 30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37 and the complement of such nucleotide sequences may be used in such methods to obtain a nucleic acid fragment encoding a substantial portion of an amino acid sequence of a polypeptide. The present invention relates to a method of obtaining a nucleic acid fragment encoding a substantial portion of a polypeptide of a gene (such as Mlo homologs) preferably a substantial portion of a plant polypeptide of a gene, comprising the steps of : synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least [one of]60 (preferably at least [one of]40, most preferably at least [one of]30) contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37, and the complement of such nucleotide sequences; and amplifying a nucleic acid fragment (preferably a cDNA inserted in a

cloning vector) using the oligonucleotide primer. The amplified nucleic acid fragment preferably will encode a portion of an Mlo homolog polypeptide.

Paragraph starting on page 19 at line 26:

cDNA clones encoding Mlo homologs were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

IN THE CLAIMS

Please cancel claims 25, 29, and 36.

Please amend claims 24, 27, 28, 31-34, and 37-39 as follows:

24. (amended) An isolated polynucleotide comprising: a) a nucleotide sequence that encodes an Mlo homolog polypeptide having a sequence identity of at least [85]90%, based on the Clustal method of alignment, when compared to a polypeptide[selected from the group consisting] of SEQ ID NO[s: SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38]:32; or b) a complement of the nucleotide sequence, wherein the complement and the nucleotide sequence have the same number of nucleotides and are 100% complementary.

27. (amended) The polynucleotide of Claim 24 wherein the amino acid sequence of the polypeptide [is selected from the group consisting of]comprises SEQ ID NO[s: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, and 38]:32.

28. (amended) The polynucleotide of Claim 24, wherein the polynucleotide comprises[is selected from] SEQ ID No[s:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, and 37]:31.

31. (amended) A cell [or a virus]comprising the recombinant DNA construct of Claim 37[polynucleotide of Claim 24].

32. (amended) The cell of Claim [33]31, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell, an insect cell, and a plant cell.

33. (amended) A transgenic plant comprising the [polynucleotide of Claim 24] recombinant DNA construct of Claim 37.

37. (amended) A [chimeric gene]recombinant DNA construct comprising the polynucleotide of Claim 24 operably linked to at least one [suitable]regulatory sequence.

38. (amended) The [chimeric gene]recombinant DNA construct of Claim [39]37, wherein the [chimeric gene]recombinant DNA construct is an expression vector.

39 (amended) A method for altering the level of expression of an Mlo homolog polypeptide [expression]in a host cell, the method comprising:

a) transforming a host cell with the [chimeric gene]recombinant DNA construct of Claim [39]37; and

b) growing the transformed cell [in]of step (a) under conditions suitable for the expression of the [chimeric gene]recombinant DNA construct wherein expression of the recombinant DNA construct results in production of altered levels of the Mlo homolog in the transformed host cell.